



<110> SAITO, Koichi

<120> Estrogen receptor genes and utilization thereof

<130> 600630-21US (561334)

<140> US 10/501,227

<141> 2004-07-12

<150> JP 2002-004395

<151> 2002-01-11

<160> 48

<210> 1

<211> 506

<212> PRT

<213> Blue Gill

<400> 1

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Arg Glu Asp Gln Cys Ala Thr Ser Asp Glu Ser Tyr Ser Val Gly Glu
35 40 45
Ser Gly Ala Gly Ala Arg Gly Phe Glu Met Ala Lys Glu Met Arg Phe
50 55 60
Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp
65 70 75 80
Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His
85 90 95
Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Arg Asn
100 105 110
Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val
115 120 125

Gly Met Met Lys Gly Gly Val Arg Lys Asp Arg Gly Arg Val Leu Arg			
130	135	140	
Arg Asp Lys Arg Arg Ala Gly Thr Asn Asp Arg Glu Lys Ala Ser Lys			
145	150	155	160
Asp Leu Glu Tyr Lys Thr Val Pro Pro Gln Asp Arg Arg Lys His Ser			
	165	170	175
Ser Ser Ser Ser Ala Gly Gly Gly Gly Gly Lys Ser Ser Val Thr Gly			
	180	185	190
Met Ser Pro Asp Gln Val Leu Leu Leu Leu Gln Gly Ala Glu Pro Pro			
	195	200	205
Met Leu Cys Ser Arg Gln Lys Leu Ser Arg Pro Tyr Thr Glu Val Thr			
	210	215	220
Ile Met Thr Leu Leu Thr Ser Met Ala Asp Lys Glu Leu Val His Met			
225	230	235	240
Ile Thr Trp Ala Lys Lys Leu Pro Gly Phe Leu Gln Leu Ser Leu His			
	245	250	255
Asp Gln Val Gln Leu Leu Glu Ser Ser Trp Leu Glu Val Leu Met Ile			
	260	265	270
Gly Leu Ile Trp Arg Ser Ile His Cys Pro Gly Lys Leu Ile Phe Ala			
	275	280	285
Gln Asp Leu Ile Leu Asp Arg Asn Glu Gly Asp Cys Val Glu Gly Phe			
	290	295	300
Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ala Ser Arg Phe Arg Met			
305	310	315	320
Leu Lys Leu Lys Pro Glu Glu Phe Val Cys Leu Lys Ala Ile Ile Leu			
	325	330	335
Leu Asn Ser Gly Ala Phe Ser Phe Cys Thr Gly Thr Met Glu Pro Leu			
	340	345	350
His Asn Ser Met Ala Val Gln Asn Met Leu Asp Thr Ile Thr Asp Ala			
	355	360	365
Leu Ile His His Ile Ser Gln Ser Gly Cys Ser Ala Gln Gln Gln Ser			
	370	375	380
Arg Arg Gln Ala Gln Leu Leu Leu Leu Leu Ser His Ile Arg His Met			
385	390	395	400
Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Lys			
	405	410	415
Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Ile			
	420	425	430

His Arg Pro Asp Arg Pro Ala Gln Phe Trp Ser Gln Ala Asp Gly Glu
 435 440 445
 Pro Pro Phe Ile Asn Asn Asn Asn Ser Ser Asn Ser Gly Ser Asn Gly
 450 455 460
 Gly Val Ser Ser Ser Val Gly Ser Ser Ser Gly Pro Arg Val Asn His
 465 470 475 480
 Glu Ser Pro Ser Arg Gly Pro Thr Gly Pro Gly Val Leu Gln Tyr Gly
 485 490 495
 Gly Ser Arg Ser Asp Cys Thr His Ile Leu
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<210> 2

<211> 3499

<212> DNA

<213> Blue Gill

<220>

<221> CDS

<222> (424)...(1944)

<400> 2

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ccctctcagt gacatgtacc ctgaagagag caggggggtcc ggaggggtag ccaactgtgga	180
ctttctggaa gggacctacg attatgccgc cccacacctt gccccgactc ctcttttacag	240
ccagtctggc tactactctg tacctctgga cgcccaaggg ccacctcag atggcagcct	300
tcagtccctg ggcagcgggc ctaccagtcc tcttgtgttt gtgccgtcca gccccagact	360
cagccccttt atgcaccgc ccagccacca ctatctggaa accacctcaa caccgtcta	420
cag atg agt ctg aaa gac tgg tta tta gga aaa gaa agg acg gtg gtg	468
Met Ser Leu Lys Asp Trp Leu Leu Gly Lys Glu Arg Thr Val Val	
1 5 10 15	
acc atg gag gag ctg agg tct agt gtc cca tcc agc cag cag cca gtt	516
Thr Met Glu Glu Leu Arg Ser Ser Val Pro Ser Ser Gln Gln Pro Val	
20 25 30	
ccc aga gag gac cag tgt gcc acc agt gat gag tcc tat agt gtg ggg	564
Pro Arg Glu Asp Gln Cys Ala Thr Ser Asp Glu Ser Tyr Ser Val Gly	
35 40 45	
gag tca ggg gct gga gcc agg ggg ttt gag atg gcc aag gag atg cgt	612

Glu Ser Gly Ala Gly Ala Arg Gly Phe Glu Met Ala Lys Glu Met Arg	
50 55 60	
ttc tgt gct gtg tgc agt gac tat gcc tct ggg tac cac tac ggg gtg	660
Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val	
65 70 75	
tgg tcc tgt gaa ggc tgt aag gcc ttc ttt aag agg agc atc cag ggt	708
Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly	
80 85 90 95	
cac aat gac tat atg tgc cca gca acc aat cag tgt act att gac agg	756
His Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Arg	
100 105 110	
aat cgg aga aag agc tgc cag gct tgc cgt ctt agg aag tgt tat gaa	804
Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu	
115 120 125	
gtg ggc atg atg aaa gga ggt gtt cgc aag gac cgt ggc cgt gtt ttg	852
Val Gly Met Met Lys Gly Gly Val Arg Lys Asp Arg Gly Arg Val Leu	
130 135 140	
cgc cgt gat aaa cga cgt gct gga acc aat gac cga gag aag gcc tct	900
Arg Arg Asp Lys Arg Arg Ala Gly Thr Asn Asp Arg Glu Lys Ala Ser	
145 150 155	
aag gac ctg gag tac aaa aca gtg ccc cct cag gac agg agg aaa cac	948
Lys Asp Leu Glu Tyr Lys Thr Val Pro Pro Gln Asp Arg Arg Lys His	
160 165 170 175	
agc agc agc agc agt gcc ggt ggt gga gga gga aaa tca tca gtg acc	996
Ser Ser Ser Ser Ser Ala Gly Gly Gly Gly Gly Lys Ser Ser Val Thr	
180 185 190	
ggg atg tct cct gac cag gtg ctc ctc ctg ctc cag ggt gcc gag ccc	1044
Gly Met Ser Pro Asp Gln Val Leu Leu Leu Leu Gln Gly Ala Glu Pro	
195 200 205	
cca atg ctg tgc tcc cgt cag aag ctg agc cga ccg tac acc gag gtc	1092
Pro Met Leu Cys Ser Arg Gln Lys Leu Ser Arg Pro Tyr Thr Glu Val	
210 215 220	
acc ata atg aca cta ctc acc agc atg gcc gat aag gag ctg gtc cac	1140
Thr Ile Met Thr Leu Leu Thr Ser Met Ala Asp Lys Glu Leu Val His	
225 230 235	
atg atc acc tgg gcc aag aag ctt cca ggt ttc ctg cag ctg tct ctc	1188
Met Ile Thr Trp Ala Lys Lys Leu Pro Gly Phe Leu Gln Leu Ser Leu	
240 245 250 255	

cat gac cag gtg cag ctg ctg gag agc tcg tgg ctg gag gtg ctg atg	1236
His Asp Gln Val Gln Leu Leu Glu Ser Ser Trp Leu Glu Val Leu Met	
260 265 270	
att ggg ctc ata tgg agg tcc atc cac tgc ccc ggc aaa ctc atc ttc	1284
Ile Gly Leu Ile Trp Arg Ser Ile His Cys Pro Gly Lys Leu Ile Phe	
275 280 285	
gca cag gac ctc ata ctg gac agg aat gaa ggt gac tgt gtg gaa ggc	1332
Ala Gln Asp Leu Ile Leu Asp Arg Asn Glu Gly Asp Cys Val Glu Gly	
290 295 300	
ttt gtt gag atc ttc gac atg ctg ctg gcc act gcc tcc cgc ttc cgc	1380
Phe Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ala Ser Arg Phe Arg	
305 310 315	
atg ctc aaa ctc aaa cct gag gag ttt gtc tgc ctc aaa gct atc atc	1428
Met Leu Lys Leu Lys Pro Glu Glu Phe Val Cys Leu Lys Ala Ile Ile	
320 325 330 335	
ctg ctc aac tct ggt gcc ttc tct ttc tgc acc ggc aca atg gag ccc	1476
Leu Leu Asn Ser Gly Ala Phe Ser Phe Cys Thr Gly Thr Met Glu Pro	
340 345 350	
ctc cac aac agc atg gca gtg cag aac atg ctg gac acc atc aca gac	1524
Leu His Asn Ser Met Ala Val Gln Asn Met Leu Asp Thr Ile Thr Asp	
355 360 365	
gct ctc ata cat cat atc agc caa tca gga tgc tcg gct cag cag cag	1572
Ala Leu Ile His His Ile Ser Gln Ser Gly Cys Ser Ala Gln Gln Gln	
370 375 380	
tcg agg cgg cag gcc cag ctg ctg ctc ctg ctc tcc cac atc agg cac	1620
Ser Arg Arg Gln Ala Gln Leu Leu Leu Leu Ser His Ile Arg His	
385 390 395	
atg agc aac aaa ggc atg gag cat ctc tac agc atg aag tgc aag aac	1668
Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn	
400 405 410 415	
aaa gtg cct ctt tac gac ctt ctg ctg gag atg ttg gac gct cac cgt	1716
Lys Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg	
420 425 430	
ata cac cgc cca gac aga cca gct cag ttc tgg tcc cag gct gac gga	1764
Ile His Arg Pro Asp Arg Pro Ala Gln Phe Trp Ser Gln Ala Asp Gly	
435 440 445	
gag cct ccc ttc att aac aac aac aac agc agc aac agt ggc agc aat	1812
Glu Pro Pro Phe Ile Asn Asn Asn Asn Ser Ser Asn Ser Gly Ser Asn	

450	455	460	
ggc ggc gtc tcc tct tca gtc ggt tcc agt tca gga ccc cga gtc aac			1860
Gly Gly Val Ser Ser Ser Val Gly Ser Ser Ser Gly Pro Arg Val Asn			
465	470	475	
cac gag agc ccg agc aga gga ccc aca ggt cca gga gtc ctg cag tac			1908
His Glu Ser Pro Ser Arg Gly Pro Thr Gly Pro Gly Val Leu Gln Tyr			
480	485	490	495
gga ggg tcc cgc tct gac tgc acc cac atc cta tga ggccgagcac aacaaa			1960
Gly Gly Ser Arg Ser Asp Cys Thr His Ile Leu			
500	505		
catctgaagg tcaaaagtaa tttttacaga tgatgtgtgt tgtacagaat gaaagctaaa			2020
ggttgtatatt taattaattt catgagataa ttatttataa attaatgat tttatagttg			2080
taactgtttt agggagtttt ttttcctttg cactaatcta gttcactaca acacgagctt			2140
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aaacaggttc aaatgaatgt gtgatttatt ttgtgtttta attccaacat cattaaagag			2440
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caaagatctg tgccacttaa acaagaatgg aaagcctcta tacaggggtca ggaaactgga			3400
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<210> 3

<211> 996
 <212> DNA
 <213> Blue Gill

<400> 3
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 atgaaaggag gtgttcgcaa ggaccgtggc cgtgttttgc gccgtgataa acgacgtgct 180
 ggaaccaatg accgagagaa ggcctctaag gacctggagt acaaaacagt gccccctcag 240
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 <211> 582
 <212> PRT
 <213> Blue Gill

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 Pro Leu Tyr Ser Gln Ser Gly Tyr Tyr Ser Val Pro Leu Asp Ala Gln
 35 40 45
 Gly Pro Pro Ser Asp Gly Ser Leu Gln Ser Leu Gly Ser Gly Pro Thr
 50 55 60
 Ser Pro Leu Val Phe Val Pro Ser Ser Pro Arg Leu Ser Pro Phe Met

65		70		75		80									
His	Pro	Pro	Ser	His	His	Tyr	Leu	Glu	Thr	Thr	Ser	Thr	Pro	Val	Tyr
				85					90					95	
Arg	Ser	Ser	Val	Pro	Ser	Ser	Gln	Gln	Pro	Val	Pro	Arg	Glu	Asp	Gln
			100					105					110		
Cys	Ala	Thr	Ser	Asp	Glu	Ser	Tyr	Ser	Val	Gly	Glu	Ser	Gly	Ala	Gly
		115					120					125			
Ala	Arg	Gly	Phe	Glu	Met	Ala	Lys	Glu	Met	Arg	Phe	Cys	Ala	Val	Cys
	130					135					140				
Ser	Asp	Tyr	Ala	Ser	Gly	Tyr	His	Tyr	Gly	Val	Trp	Ser	Cys	Glu	Gly
145				150					155					160	
Cys	Lys	Ala	Phe	Phe	Lys	Arg	Ser	Ile	Gln	Gly	His	Asn	Asp	Tyr	Met
			165					170					175		
Cys	Pro	Ala	Thr	Asn	Gln	Cys	Thr	Ile	Asp	Arg	Asn	Arg	Arg	Lys	Ser
		180						185					190		
Cys	Gln	Ala	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Val	Gly	Met	Met	Lys
	195						200					205			
Gly	Gly	Val	Arg	Lys	Asp	Arg	Gly	Arg	Val	Leu	Arg	Arg	Asp	Lys	Arg
	210					215					220				
Arg	Ala	Gly	Thr	Asn	Asp	Arg	Glu	Lys	Ala	Ser	Lys	Asp	Leu	Glu	Tyr
225				230					235					240	
Lys	Thr	Val	Pro	Pro	Gln	Asp	Arg	Arg	Lys	His	Ser	Ser	Ser	Ser	Ser
			245					250					255		
Ala	Gly	Gly	Gly	Gly	Gly	Lys	Ser	Ser	Val	Thr	Gly	Met	Ser	Pro	Asp
		260						265				270			
Gln	Val	Leu	Leu	Leu	Leu	Gln	Gly	Ala	Glu	Pro	Pro	Met	Leu	Cys	Ser
	275						280					285			
Arg	Gln	Lys	Leu	Ser	Arg	Pro	Tyr	Thr	Glu	Val	Thr	Ile	Met	Thr	Leu
	290					295					300				
Leu	Thr	Ser	Met	Ala	Asp	Lys	Glu	Leu	Val	His	Met	Ile	Thr	Trp	Ala
305				310					315					320	
Lys	Lys	Leu	Pro	Gly	Phe	Leu	Gln	Leu	Ser	Leu	His	Asp	Gln	Val	Gln
			325					330				335			
Leu	Leu	Glu	Ser	Ser	Trp	Leu	Glu	Val	Leu	Met	Ile	Gly	Leu	Ile	Trp
		340					345					350			
Arg	Ser	Ile	His	Cys	Pro	Gly	Lys	Leu	Ile	Phe	Ala	Gln	Asp	Leu	Ile
	355						360					365			
Leu	Asp	Arg	Asn	Glu	Gly	Asp	Cys	Val	Glu	Gly	Phe	Val	Glu	Ile	Phe

370		375		380
Asp Met Leu Leu Ala Thr Ala Ser Arg Phe Arg Met Leu Lys Leu Lys				
385		390		400
Pro Glu Glu Phe Val Cys Leu Lys Ala Ile Ile Leu Leu Asn Ser Gly				
	405		410	415
Ala Phe Ser Phe Cys Thr Gly Thr Met Glu Pro Leu His Asn Ser Met				
	420		425	430
Ala Val Gln Asn Met Leu Asp Thr Ile Thr Asp Ala Leu Ile His His				
	435		440	445
Ile Ser Gln Ser Gly Cys Ser Ala Gln Gln Gln Ser Arg Arg Gln Ala				
	450		455	460
Gln Leu Leu Leu Leu Leu Ser His Ile Arg His Met Ser Asn Lys Gly				
465		470		480
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Lys Val Pro Leu Tyr				
	485		490	495
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Ile His Arg Pro Asp				
	500		505	510
Arg Pro Ala Gln Phe Trp Ser Gln Ala Asp Gly Glu Pro Pro Phe Ile				
	515		520	525
Asn Asn Asn Asn Ser Ser Asn Ser Gly Ser Asn Gly Gly Val Ser Ser				
	530		535	540
Ser Val Gly Ser Ser Ser Gly Pro Arg Val Asn His Glu Ser Pro Ser				
545		550		560
Arg Gly Pro Thr Gly Pro Gly Val Leu Gln Tyr Gly Gly Ser Arg Ser				
	565		570	575
Asp Cys Thr His Ile Leu				
	580			

<210> 5

<211> 1824

<212> DNA

<213> Blue Gill

<220>

<221> CDS

<222> (74)...(1822)

<400> 5

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Met Tyr Pro Glu Glu Ser Arg Gly Ser Gly Gly Val	
1 5 10	
gcc act gtg gac ttt ctg gaa ggg acc tac gat tat gcc gcc ccc acc	157
Ala Thr Val Asp Phe Leu Glu Gly Thr Tyr Asp Tyr Ala Ala Pro Thr	
15 20 25	
cct gcc ccg act cct ctt tac agc cag tct ggc tac tac tct gta cct	205
Pro Ala Pro Thr Pro Leu Tyr Ser Gln Ser Gly Tyr Tyr Ser Val Pro	
30 35 40	
ctg gac gcc caa ggg cca ccc tca gat ggc agc ctt cag tcc ctg ggc	253
Leu Asp Ala Gln Gly Pro Pro Ser Asp Gly Ser Leu Gln Ser Leu Gly	
45 50 55 60	
agc ggg cct acc agt cct ctt gtg ttt gtg ccg tcc agc ccc aga ctc	301
Ser Gly Pro Thr Ser Pro Leu Val Phe Val Pro Ser Ser Pro Arg Leu	
65 70 75	
agc ccc ttt atg cac ccg ccc agc cac cac tat ctg gaa acc acc tca	349
Ser Pro Phe Met His Pro Pro Ser His His Tyr Leu Glu Thr Thr Ser	
80 85 90	
aca ccc gtc tac agg tct agt gtc cca tcc agc cag cag cca gtt ccc	397
Thr Pro Val Tyr Arg Ser Ser Val Pro Ser Ser Gln Gln Pro Val Pro	
95 100 105	
aga gag gac cag tgt gcc acc agt gat gag tcc tat agt gtg ggg gag	445
Arg Glu Asp Gln Cys Ala Thr Ser Asp Glu Ser Tyr Ser Val Gly Glu	
110 115 120	
tca ggg gct gga gcc agg ggg ttt gag atg gcc aag gag atg cgt ttc	493
Ser Gly Ala Gly Ala Arg Gly Phe Glu Met Ala Lys Glu Met Arg Phe	
125 130 135 140	
tgt gct gtg tgc agt gac tat gcc tct ggg tac cac tac ggg gtg tgg	541
Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp	
145 150 155	
tcc tgt gaa ggc tgt aag gcc ttc ttt aag agg agc atc cag ggt cac	589
Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His	
160 165 170	
aat gac tat atg tgc cca gca acc aat cag tgt act att gac agg aat	637
Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Arg Asn	
175 180 185	
cgg aga aag agc tgc cag gct tgc cgt ctt agg aag tgt tat gaa gtg	685

Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val	
190 195 200	
ggc atg atg aaa gga ggt gtt cgc aag gac cgt ggc cgt gtt ttg cgc	733
Gly Met Met Lys Gly Gly Val Arg Lys Asp Arg Gly Arg Val Leu Arg	
205 210 215 220	
cgt gat aaa cga cgt gct gga acc aat gac cga gag aag gcc tct aag	781
Arg Asp Lys Arg Arg Ala Gly Thr Asn Asp Arg Glu Lys Ala Ser Lys	
225 230 235	
gac ctg gag tac aaa aca gtg ccc cct cag gac agg agg aaa cac agc	829
Asp Leu Glu Tyr Lys Thr Val Pro Pro Gln Asp Arg Arg Lys His Ser	
240 245 250	
agc agc agc agt gcc ggt ggt gga gga gga aaa tca tca gtg acc ggg	877
Ser Ser Ser Ser Ala Gly Gly Gly Gly Gly Lys Ser Ser Val Thr Gly	
255 260 265	
atg tct cct gac cag gtg ctc ctc ctg ctc cag ggt gcc gag ccc cca	925
Met Ser Pro Asp Gln Val Leu Leu Leu Leu Gln Gly Ala Glu Pro Pro	
270 275 280	
atg ctg tgc tcc cgt cag aag ctg agc cga ccg tac acc gag gtc acc	973
Met Leu Cys Ser Arg Gln Lys Leu Ser Arg Pro Tyr Thr Glu Val Thr	
285 290 295 300	
ata atg aca cta ctc acc agc atg gcc gat aag gag ctg gtc cac atg	1021
Ile Met Thr Leu Leu Thr Ser Met Ala Asp Lys Glu Leu Val His Met	
305 310 315	
atc acc tgg gcc aag aag ctt cca ggt ttc ctg cag ctg tct ctc cat	1069
Ile Thr Trp Ala Lys Lys Leu Pro Gly Phe Leu Gln Leu Ser Leu His	
320 325 330	
gac cag gtg cag ctg ctg gag agc tcg tgg ctg gag gtg ctg atg att	1117
Asp Gln Val Gln Leu Leu Glu Ser Ser Trp Leu Glu Val Leu Met Ile	
335 340 345	
ggg ctc ata tgg agg tcc atc cac tgc ccc ggc aaa ctc atc ttc gca	1165
Gly Leu Ile Trp Arg Ser Ile His Cys Pro Gly Lys Leu Ile Phe Ala	
350 355 360	
cag gac ctc ata ctg gac agg aat gaa ggt gac tgt gtg gaa ggc ttt	1213
Gln Asp Leu Ile Leu Asp Arg Asn Glu Gly Asp Cys Val Glu Gly Phe	
365 370 375 380	
gtt gag atc ttc gac atg ctg ctg gcc act gcc tcc cgc ttc cgc atg	1261
Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ala Ser Arg Phe Arg Met	
385 390 395	

ctc aaa ctc aaa cct gag gag ttt gtc tgc ctc aaa gct atc atc ctg	1309
Leu Lys Leu Lys Pro Glu Glu Phe Val Cys Leu Lys Ala Ile Ile Leu	
400 405 410	
ctc aac tct ggt gcc ttc tct ttc tgc acc ggc aca atg gag ccc ctc	1357
Leu Asn Ser Gly Ala Phe Ser Phe Cys Thr Gly Thr Met Glu Pro Leu	
415 420 425	
cac aac agc atg gca gtg cag aac atg ctg gac acc atc aca gac gct	1405
His Asn Ser Met Ala Val Gln Asn Met Leu Asp Thr Ile Thr Asp Ala	
430 435 440	
ctc ata cat cat atc agc caa tca gga tgc tcg gct cag cag cag tcg	1453
Leu Ile His His Ile Ser Gln Ser Gly Cys Ser Ala Gln Gln Gln Ser	
445 450 455 460	
agg cgg cag gcc cag ctg ctg ctc ctg ctc tcc cac atc agg cac atg	1501
Arg Arg Gln Ala Gln Leu Leu Leu Leu Leu Ser His Ile Arg His Met	
465 470 475	
agc aac aaa ggc atg gag cat ctc tac agc atg aag tgc aag aac aaa	1549
Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Lys	
480 485 490	
gtg cct ctt tac gac ctt ctg ctg gag atg ttg gac gct cac cgt ata	1597
Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Ile	
495 500 505	
cac cgc cca gac aga cca gct cag ttc tgg tcc cag gct gac gga gag	1645
His Arg Pro Asp Arg Pro Ala Gln Phe Trp Ser Gln Ala Asp Gly Glu	
510 515 520	
cct ccc ttc att aac aac aac aac agc agc aac agt ggc agc aat ggc	1693
Pro Pro Phe Ile Asn Asn Asn Asn Ser Ser Asn Ser Gly Ser Asn Gly	
525 530 535 540	
ggc gtc tcc tct tca gtc ggt tcc agt tca gga ccc cga gtc aac cac	1741
Gly Val Ser Ser Ser Val Gly Ser Ser Ser Gly Pro Arg Val Asn His	
545 550 555	
gag agc ccg agc aga gga ccc aca ggt cca gga gtc ctg cag tac gga	1789
Glu Ser Pro Ser Arg Gly Pro Thr Gly Pro Gly Val Leu Gln Tyr Gly	
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<211> 62

<212> DNA

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ag 62

<210> 13

<211> 24

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<213> Artificial Sequence

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<211> 39

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<211> 38

<212> DNA

<213> Artificial Sequence

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 <400> 23

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Ser	Pro	Leu	Glu	Arg	Ser	Gln	Pro	Ile	Cys	Ile	Pro	Ser	Pro	Tyr	Thr
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Asp	Leu	Ser	His	Asp	Phe	Thr	Thr	Ile	Pro	Phe	Tyr	Ser	Pro	Thr	Phe
	50					55					60				
Phe	Ser	Tyr	Ala	Ser	Pro	Gly	Ile	Ser	Asp	Cys	Pro	Ser	Val	His	Gln
65					70					75				80	
Ser	Leu	Ser	Pro	Ser	Leu	Phe	Trp	Pro	Ser	His	Gly	His	Val	Gly	Ser
				85					90					95	
Pro	Ile	Pro	Leu	His	His	Ser	Gln	Pro	Arg	Pro	Gln	His	Arg	Gln	Pro
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Ile	Gln	Ser	Pro	Trp	Val	Glu	Leu	Ser	Pro	Leu	Glu	Ser	Thr	Leu	Thr
		115					120					125			
Thr	Ser	Lys	Ser	Val	Arg	Arg	Arg	Ser	Gln	Glu	Ser	Glu	Asp	Gly	Val
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Val	Ser	Ser	Gly	Gly	Lys	Ala	Asp	Ile	His	Tyr	Cys	Ala	Val	Cys	His
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Lys	Ala	Phe	Phe	Lys	Arg	Ser	Ile	Gln	Arg	His	Asn	Asp	Tyr	Ile	Cys
		180						185					190		
Pro	Ala	Thr	Asn	Gln	Cys	Thr	Ile	Asp	Lys	Asn	Arg	Arg	Lys	Ser	Cys
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Val	Thr	Arg	Leu	Ser	Thr	Gln	Gly	Arg	Thr	Asn	Arg	Thr	Ala	Val	Leu
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Thr	Gly	Pro	Ala	Val	Gly	Ser	Leu	Ile	Ser	Leu	Asn	Ser	Pro	Ala	Leu
		260						265					270		
Thr	Pro	Glu	Gln	Leu	Ile	Glu	Arg	Ile	Ile	Asp	Ala	Glu	Pro	Pro	Glu
		275					280					285			
Ile	Tyr	Leu	Met	Lys	Asp	Met	Arg	Arg	Pro	Leu	Thr	Glu	Ala	Asn	Val
	290						295					300			

Met Met Ser Leu Thr Asn Leu Ala Asp Lys Glu Leu Val His Met Ile
 305 310 315 320
 Ser Trp Ala Lys Lys Ile Pro Gly Phe Val Glu Leu Ser Leu Leu Asp
 325 330 335
 Gln Val His Leu Leu Glu Cys Cys Trp Leu Glu Val Leu Met Val Gly
 340 345 350
 Leu Met Trp Arg Ser Val Asp His Pro Gly Lys Leu Ile Phe Ser Arg
 355 360 365
 Asp Leu Ser Leu Ser Arg Glu Glu Gly Ser Cys Val Gln Gly Phe Ala
 370 375 380
 Glu Ile Phe Asp Met Leu Ile Ala Ala Thr Ser Arg Val Arg Glu Leu
 385 390 395 400
 Lys Leu Gln Arg Glu Glu Tyr Val Cys Leu Lys Ala Met Ile Leu Leu
 405 410 415
 Asn Ser Asn Met Cys Leu Gly Ser Ser Glu Gly Ser Glu Glu Leu Gln
 420 425 430
 Ser Arg Ser Lys Leu Leu Cys Leu Leu Asp Ala Val Thr Asp Ala Leu
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 Val Trp Ala Ile Ala Lys Thr Gly Leu Thr Phe Arg Gln Gln Tyr Thr
 450 455 460
 Arg Leu Ala His Leu Leu Met Leu Leu Ser His Ile Arg His Val Ser
 465 470 475 480
 Asn Lys Gly Met Asp His Leu His Cys Met Lys Met Lys Asn Met Val
 485 490 495
 Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu Asp Ala His Ile Met His
 500 505 510
 Ser Ser Arg Leu Ser His Gln Pro Ile Gln Gln Asp Ala Gln Asp Gln
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Met Ala Cys Ser

1

cca gag aag gat cag ccc ctc ctc cag ctc cag aag gtg gac tcc agt 165
Pro Glu Lys Asp Gln Pro Leu Leu Gln Leu Gln Lys Val Asp Ser Ser

5 10 15 20

cga gtt ggc agt cgt gtc gtc tcc ccg atc ctc aac tcc ccg ttg gaa 213
Arg Val Gly Ser Arg Val Val Ser Pro Ile Leu Asn Ser Pro Leu Glu

25 30 35

aga agc cag ccc atc tgc atc ccc tcc cct tac acc gac ctc agc cac 261
Arg Ser Gln Pro Ile Cys Ile Pro Ser Pro Tyr Thr Asp Leu Ser His

40 45 50

gac ttc acc acc ata cct ttc tac agt cca act ttc ttt agt tat gcc 309
Asp Phe Thr Thr Ile Pro Phe Tyr Ser Pro Thr Phe Phe Ser Tyr Ala

55 60 65

agt cca ggc att tca gac tgc ccc tcc gtc cat cag tca cta agc ccc 357
Ser Pro Gly Ile Ser Asp Cys Pro Ser Val His Gln Ser Leu Ser Pro

70 75 80

tcc tta ttc tgg ccc agc cat ggc cat gtt ggg tcc ccc ata ccc ctg 405

Ser Leu Phe Trp Pro Ser His Gly His Val Gly Ser Pro Ile Pro Leu
85 90 95 100

cac cac tcc cag cct cga cct cag cac aga cag cca atc cag agt cca 453
His His Ser Gln Pro Arg Pro Gln His Arg Gln Pro Ile Gln Ser Pro

105 110 115

tgg gtg gag ttg tca cca ctg gag agc acc tta aca acc agt aag agt 501
Trp Val Glu Leu Ser Pro Leu Glu Ser Thr Leu Thr Thr Ser Lys Ser

120 125 130

gta agg agg cgt tct cag gag agc gag gat ggc gtg gtg tcg tcc ggc 549
Val Arg Arg Arg Ser Gln Glu Ser Glu Asp Gly Val Val Ser Ser Gly

135 140 145

ggg aag gcg gac atc cac tac tgc gct gtg tgt cac gac tac gcc tca 597

Gly Lys Ala Asp Ile His Tyr Cys Ala Val Cys His Asp Tyr Ala Ser	
150	155
gga tac cac tac ggc gtc tgg tca tgt gag ggg tgt aag gcc ttc ttc	645
Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe	
165	170
aag agg agc atc caa aga cac aat gac tac atc tgc cca gca acc aat	693
Lys Arg Ser Ile Gln Arg His Asn Asp Tyr Ile Cys Pro Ala Thr Asn	
185	190
caa tgc act ata gac aag aac cgc cgt aag agc tgc cag gcg tgc cgc	741
Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg	
200	205
ctt cgc aaa tgc aat gaa gtt ggc atg acc aag tgt ggt gtg aga aag	789
Leu Arg Lys Cys Asn Glu Val Gly Met Thr Lys Cys Gly Val Arg Lys	
215	220
gag cgt ggg aac tgc aga aac ccc cag atg agg cga gtg acc cga ctc	837
Glu Arg Gly Asn Cys Arg Asn Pro Gln Met Arg Arg Val Thr Arg Leu	
230	235
tcc aca cag ggc aga act aac aga aca gct gtg tta act gga cca gcc	885
Ser Thr Gln Gly Arg Thr Asn Arg Thr Ala Val Leu Thr Gly Pro Ala	
245	250
gtg ggt tca cta atc tcg ctc aac tct cct gca ctg acc cca gag cag	933
Val Gly Ser Leu Ile Ser Leu Asn Ser Pro Ala Leu Thr Pro Glu Gln	
265	270
ctg att gaa cga ata att gat gct gag cca cca gag atc tac ctc atg	981
Leu Ile Glu Arg Ile Ile Asp Ala Glu Pro Pro Glu Ile Tyr Leu Met	
280	285
aaa gac atg agg agg cct ctg act gaa gca aac gtc atg atg tcg ctc	1029
Lys Asp Met Arg Arg Pro Leu Thr Glu Ala Asn Val Met Met Ser Leu	
295	300
aca aac ctt gct gat aag gag ctg gtt cac atg atc agc tgg gcc aag	1077
Thr Asn Leu Ala Asp Lys Glu Leu Val His Met Ile Ser Trp Ala Lys	
310	315
aag att cca ggg ttt gta gag ctc agt ctc ttg gac cag gtg cac ctg	1125
Lys Ile Pro Gly Phe Val Glu Leu Ser Leu Leu Asp Gln Val His Leu	
325	330
ttg gag tgc tgc tgg ctg gag gtg ctg atg gtt gga ctg atg tgg agg	1173
Leu Glu Cys Cys Trp Leu Glu Val Leu Met Val Gly Leu Met Trp Arg	
345	350
	355

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Ser Val Asp His Pro Gly Lys Leu Ile Phe Ser Arg Asp Leu Ser Leu	
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Ser Arg Glu Glu Gly Ser Cys Val Gln Gly Phe Ala Glu Ile Phe Asp	
375 380 385	
atg ctg ata gct gcc acg tcc agg gtg aga gag ctc aag ctc cag agg	1317
Met Leu Ile Ala Ala Thr Ser Arg Val Arg Glu Leu Lys Leu Gln Arg	
390 395 400	
gag gag tac gtc tgc ctc aag gcc atg atc ctc ctt aac tcc aac atg	1365
Glu Glu Tyr Val Cys Leu Lys Ala Met Ile Leu Leu Asn Ser Asn Met	
405 410 415 420	
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Cys Leu Gly Ser Ser Glu Gly Ser Glu Glu Leu Gln Ser Arg Ser Lys	
425 430 435	
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Leu Leu Cys Leu Leu Asp Ala Val Thr Asp Ala Leu Val Trp Ala Ile	
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gcc aaa act ggc ctc act ttc cgc caa cag tac acc cgc ctc gcc cac	1509
Ala Lys Thr Gly Leu Thr Phe Arg Gln Gln Tyr Thr Arg Leu Ala His	
455 460 465	
ctg ctt atg ctg ctc tca cac atc cgc cat gtc agt aac aaa ggc atg	1557
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470 475 480	
gac cac ctc cac tgc atg aaa atg aag aac atg gtg cct ttg tat gac	1605
Asp His Leu His Cys Met Lys Met Lys Asn Met Val Pro Leu Tyr Asp	
485 490 495 500	
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Leu Leu Leu Glu Met Leu Asp Ala His Ile MET His Ser Ser Arg Leu	
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tct cac cag ccc ata cag caa gac gca cag gac cag agg gag gct cct	1701
Ser His Gln Pro Ile Gln Gln Asp Ala Gln Asp Gln Arg Glu Ala Pro	
520 525 530	
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Ala Arg Pro His Ser Cys Gly Ser Gly Pro Leu Asn Thr Trp Thr Pro	
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550

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<400> 29

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<210> 39

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 39

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<210> 40

<211> 20

<212> DNA

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<220>

<223> Designed oligonucleotide primer for PCR

<400> 40

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<212> DNA

<213> Blue gill

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cgtgtcgtct	ccccgatcct	caactccccg	ttggaagaag	ccagcccata	tgcaccccct	180
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ccttattctg	gccagccat	ggccatgttg	ggcccccat	acccctgcac	cactcccagc	360
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<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

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<210> 44

<211> 139

<212> DNA

<213> Blue gill

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